

SEQUENCE LISTING

<110> BAGUTTI; Claudia
 CHIQUET-EHRISMANN; Ruth
 DRABIKOWSKI; Krzysztof; Piotr
 RUBIN-LUCHT; Beatrix; Paulette

<120> METHODS FOR DETECTING TENEURIN
 SIGNALLING AND RELATED SCREENING METHODS

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<140> 10/530,542

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<151> 2003-10-14

<150> GB0223984

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Gly	Arg	Lys	Pro	Arg	Gln	Ser	Tyr	Asn	Ser	Arg	Glu	Thr	Leu	His	Glu	
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Lys	Glu	Val	Glu	Lys	Ser	Thr	Gln	Glu	Met	Glu	Phe	Cys	Glu	Thr	Ser	
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cac	act	ctg	tgc	tct	ggc	tac	caa	aca	gac	atg	cac	agc	gtt	tct	cgg	288
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ggt gct gcc tca cct gac cat gca cta aga atg tgg ata agg gga atg	384
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aaa tca gag cat agt tcc tgt ttg tcc agc cgg gcc aac tct gca tta	432
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tcc ttg act gac act gac cat gaa agg aag tct gat ggg gaa aat gat	480
Ser Leu Thr Asp Thr Asp His Glu Arg Lys Ser Asp Gly Glu Asn Asp	
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Pro Pro Pro Pro Pro His Ala Cys Thr Cys Ala Arg Lys Pro Pro Pro	
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gca gcg gac tct ctt cag agg aga tca atg act acc cgc agc cag ccc	624
Ala Ala Asp Ser Leu Gln Arg Arg Ser Met Thr Thr Arg Ser Gln Pro	
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Ser Pro Ala Ala Pro Ala Pro Pro Thr Ser Thr Gln Asp Ser Val His	
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Pro Arg Pro Leu Pro Arg Ser Thr Phe Ser Arg Pro Ala Phe Thr Phe	
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 Lys Glu Val Glu Lys Ser Thr Gln Glu Met Glu Phe Cys Glu Thr Ser
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 His Thr Leu Cys Ser Gly Tyr Gln Thr Asp Met His Ser Val Ser Arg
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 His Gly Tyr Gln Leu Glu Met Gly Ser Asp Val Asp Thr Glu Thr Glu
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 Gly Ala Ala Ser Pro Asp His Ala Leu Arg Met Trp Ile Arg Gly Met
 115 120 125
 Lys Ser Glu His Ser Ser Cys Leu Ser Ser Arg Ala Asn Ser Ala Leu
 130 135 140
 Ser Leu Thr Asp Thr Asp His Glu Arg Lys Ser Asp Gly Glu Asn Asp
 145 150 155 160
 Val Gln Ser Ser Pro His Asn Gln Phe Thr Phe Arg Pro Leu Pro Pro
 165 170 175
 Pro Pro Pro Pro Pro His Ala Cys Thr Cys Ala Arg Lys Pro Pro Pro
 180 185 190
 Ala Ala Asp Ser Leu Gln Arg Arg Ser Met Thr Thr Arg Ser Gln Pro
 195 200 205
 Ser Pro Ala Ala Pro Ala Pro Pro Thr Ser Thr Gln Asp Ser Val His
 210 215 220
 Leu His Asn Ser Trp Val Leu Asn Ser Asn Ile Pro Leu Glu Thr Arg
 225 230 235 240
 His Phe Leu Phe Lys His Gly Ser Gly Ser Ser Ala Ile Phe Ser Ala
 245 250 255
 Ala Ser Gln Asn Tyr Pro Leu Thr Ser Asn Thr Val Tyr Ser Pro Pro
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 Pro Arg Pro Leu Pro Arg Ser Thr Phe Ser Arg Pro Ala Phe Thr Phe
 275 280 285
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Arg Val Pro Thr Gln Lys Ser Tyr Ser Ser Ser Glu Thr Leu Lys Ala	
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tat gac cat gac agc agg atg cac tat gga aac cga gtc aca gac ctc	192
Tyr Asp His Asp Ser Arg Met His Tyr Gly Asn Arg Val Thr Asp Leu	
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Cys Ser Asp Met Gly Ile Leu His Gln Gly Tyr Ser Leu Ser Thr Gly	
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115 120 125	
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Pro Pro Val Ser Cys Gln Met Pro Leu Leu Asp Ser Asn Thr Ser His	
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Gln Ile Met Asp Thr Asn Pro Asp Glu Glu Phe Ser Pro Asn Ser Tyr	
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Phe Lys Thr Ser Ser Gly Ser Thr Pro Leu Phe Ser Ser Ser Ser Pro	
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 Ile His Arg Glu Ser Asp Glu Phe Pro Arg Gln Gly Thr Asn Phe Thr
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 Leu Ala Glu Leu Gly Ile Cys Glu Pro Ser Pro His Arg Ser Gly Tyr
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 Cys Ser Asp Met Gly Ile Leu His Gln Gly Tyr Ser Leu Ser Thr Gly

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Leu Ala Phe Cys Ala Glu Met Gly Leu Pro His Arg Gly Tyr Ser Ile	
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Ser Ala Gly Ser Asp Ala Asp Thr Glu Asn Glu Ala Val Met Ser Pro	
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Glu His Ala Met Arg Leu Trp Gly Arg Gly Val Lys Ser Gly Arg Ser	
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Ser Cys Leu Ser Ser Arg Ser Asn Ser Ala Leu Thr Leu Thr Asp Thr	
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Glu His Glu Asn Lys Ser Asp Ser Glu Asn Glu Gln Pro Ala Ser Asn	
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caa ggc cag tct acc ctg cag ccc ttg ccg cct tcc cat aag cag cac	576
Gln Gly Gln Ser Thr Leu Gln Pro Leu Pro Pro Ser His Lys Gln His	
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tct gca cag cat cat cca tcc atc act tct ctc aac aga aac tcc ctg	624
Ser Ala Gln His His Pro Ser Ile Thr Ser Leu Asn Arg Asn Ser Leu	
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acc aat aga agg aac cag agt ccg gcc ccg ccg gct gct ttg ccc gcc	672
Thr Asn Arg Arg Asn Gln Ser Pro Ala Pro Pro Ala Ala Leu Pro Ala	
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Glu Leu Gln Thr Thr Pro Glu Ser Val Gln Leu Gln Asp Ser Trp Val	
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Leu Gly Ser Asn Val Pro Leu Glu Ser Arg His Phe Leu Phe Lys Thr	
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gga aca ggt aca acg cca ctg ttc agt act gca acc cca gga tac aca	816
Gly Thr Gly Thr Thr Pro Leu Phe Ser Thr Ala Thr Pro Gly Tyr Thr	
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Met Ala Ser Gly Ser Val Tyr Ser Pro Pro Thr Arg Pro Leu Pro Arg	
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ctg	gca	ata	ctc	ctg	tct	tat	ttt	ata	gca	atg						993
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Cys	Arg	Val	Pro	Thr	Gln	Lys	Ser	Tyr	Ser	Ser	Ser	Glu	Thr	Leu	Lys
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Phe	Thr	Leu	Arg	Gln	Leu	Gly	Val	Cys	Glu	Pro	Ala	Thr	Arg	Arg	Gly
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 Lys Ala Pro Gln Lys Ser Tyr Ser Ser Ser Glu Thr Leu Lys Ala Tyr
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 gac cag gac gcc cgc cta gcc tat ggc agc cgc gtc aag gac att gtg 192
 Asp Gln Asp Ala Arg Leu Ala Tyr Gly Ser Arg Val Lys Asp Ile Val
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 Pro Gln Glu Ala Glu Gaa Phe Cys Arg Thr Gly Ala Asn Phe Thr Leu
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 cgg gag ctg ggg ctg gaa gaa gta acg ccc cct cac ggg acc ctg tac 288
 Arg Glu Leu Gly Leu Glu Glu Val Thr Pro Pro His Gly Thr Leu Tyr
 85 90 95
 cgg aca gac att ggc ctc ccc cac tgc ggc tac tcc atg ggg gct ggc 336
 Arg Thr Asp Ile Gly Leu Pro His Cys Gly Tyr Ser Met Gly Ala Gly
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 tct gat gcc gac atg gag gct gac acg gtg ctg tcc cct gag cac ccc 384
 Ser Asp Ala Asp Met Glu Ala Asp Thr Val Leu Ser Pro Glu His Pro
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 gtg cgt ctg tgg ggc cgg agc aca cgg tca ggg cgc agc tcc tgc ctg 432
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 aac act gag act gat cat ccg ggc ggc ctg cag aac cac gcg cgg ctc 528
 Asn Thr Glu Thr Asp His Pro Gly Gly Leu Gln Asn His Ala Arg Leu
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 Arg Thr Pro Pro Pro Pro Leu Ser His Ala His Thr Pro Asn Gln His
 180 185 190

cac gcg gcc tcc att aac tcc ctg aac cgg ggc aac ttc acg ccg agg	624
His Ala Ala Ser Ile Asn Ser Leu Asn Arg Gly Asn Phe Thr Pro Arg	
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Ser Asn Pro Ser Pro Ala Pro Thr Asp His Ser Leu Ser Gly Glu Pro	
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Pro Ala Gly Gly Ala Gln Glu Pro Ala His Ala Gln Glu Asn Trp Leu	
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Leu Asn Ser Asn Ile Pro Leu Glu Thr Arg Asn Leu Gly Lys Gln Pro	
245 250 255	
ttc cta ggg aca ttg cag gac aac ctc att gag atg gac att ctc ggc	816
Phe Leu Gly Thr Leu Gln Asp Asn Leu Ile Glu Met Asp Ile Leu Gly	
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Ala Ser Arg His Asp Gly Ala Tyr Ser Asp Gly His Phe Leu Phe Lys	
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Pro Gly Gly Thr Ser Pro Leu Phe Cys Thr Thr Ser Pro Gly Tyr Pro	
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<223> PCR primer for 4 Kb upstream of promoter

<400> 11
cattggtcaa ttggcgcgcc cattcgcaga cg

32

<210> 12
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide primer

<221> primer_bind
<222> (1)...(26)
<223> PCR primer for 4 Kb upstream of promoter

<400> 12
attaggcggg ggggggtaccg cattcg

26

<210> 13
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide primer

<221> primer_bind
<222> (1)...(26)
<223> PCR primer for 3 Kb downstream of promoter

<400> 13
gaattcgcat gcaaattgtga agcatg

26

<210> 14
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide primer

<221> primer_bind

<222> (1)...(27)
 <223> PCR primer for 3 Kb downstream of promoter

 <400> 14
 ccaccaggta ccggatcacc attgttc 27

 <210> 15
 <211> 26
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Oligonucleotide primer

 <221> primer_bind
 <222> (1)...(26)
 <223> PCR primer for DNA encoding the long intracellular
 domain

 <400> 15
 cagagtgcgg ccgcccgtgc gtttcg 26

 <210> 16
 <211> 27
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Oligonucleotide primer

 <221> primer_bind
 <222> (1)...(27)
 <223> PCR primer for DNA encoding the long intracellular
 domain

 <400> 16
 ggctaggaat tcattccatt tggatgg 27

 <210> 17
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Oligonucleotide primer

 <221> primer_bind
 <222> (1)...(30)
 <223> PCR primer for DNA encoding the short
 intracellular domain

 <400> 17
 ttacaatttt tcaggcggcc gcaagttggc 30

 <210> 18
 <211> 27
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Oligonucleotide primer

<221> primer_bind
<222> (1)...(27)
<223> PCR primer for DNA encoding the short
intracellular domain

<400> 18
ggctaggaat tcattccatt tggatgg

27

<210> 19
<211> 20
<212> PRT
<213> Homo sapiens

<220>
<221> PEPTIDE
<222> (1)...(20)
<223> Ten-1 specific peptide from the N-terminus of the
long variant

<400> 19
Met Phe Gln His Arg Thr Thr Asn Ala Gln Gly Pro Pro Pro Asn Arg
1 5 10 15
Pro Met Pro Arg
20

<210> 20
<211> 20
<212> PRT
<213> Homo sapiens

<220>
<221> PEPTIDE
<222> (1)...(20)
<223> Ten-1 specific peptides from the common C-terminus

<400> 20
Pro Ala His Gln Ser Gly Leu Leu Ala Ser Val His Ser Trp Lys Phe
1 5 10 15
Arg Lys Ser Glu
20